SEQUENCE LISTING

<110> Springer, Timothy A.
      Shimaoka, Motomu
      Lu, Chafen

<120> MODIFIED POLYPEPTIDES STABILIZED IN A
      DESIRED CONFORMATION AND METHODS FOR PRODUCING SAME

<130> CBN-002CP

<150> US 60/229,700
<151> 2000-09-01

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 5133
<212> DNA
<213> Homo sapiens

<400> 1
cctctttcac cctgtctagg ttgccagcaa atcccacggg cctcctgacg ctgcccctgg 60
ggccacaggt ccctcgagtg ctggaaggat gaaggattcc tgcatcactg tgatggccat 120
ggcgctgctg tctgggttct ttttcttcgc gccggcctcg agctacaacc tggacgtgcg 180
gggcgcgcgg agcttctccc caccgcgcgc cggcgaggcac tttggatacc gcgtcctgca 240
ggtcggaaac ggggtcatcg tgggagctcc aggggaggg aacagcacag gaagcctcta 300
tcagtgccag tcgggcacag gacactgcct gccagtcacc ctgagaggtt ccaactatac 360
ctccaagtac ttgggaatga ccttggcaac agaccccaca gatggaagca ttttggcctg 420
tgacccctggg ctgtctcgaa cgtgtgacca gaacacctat ctgagtggcc tgtgttacct 480
cttccgccag aatctgcagg gtcccatgct gcaggggcgc cctggttttc aggaatgtat 540
caagggcaac gtagacctgg tatttctgtt tgatggttcg atgagcttgc agccagatga 600
atttcagaaa attctggact tcatgaagga tgtgatgaag aaactcagca acacttcgta 660
ccagtttgct gctgttcagt tttccacaag ctacaaaaca gaatttgatt tctcagatta 720
tgttaaatgg aaggaccctg atgctctgct gaagcatgta aagcacatgt tgctgttgac 780
caataccttt ggtgccatca attatgtcgc gacagaggtg ttccgggagg agctgggggc 840
ccggccagat gccaccaaag tgcttatcat catcacggat gggaggccca ctgacagtgg 900
caacatcgat gcggccaaag acatcatccg ctacatcatc gggattggaa agcattttca 960
gaccaaggag agtcaggaga ccctccacaa atttgcatca aaaccgcga gcgagtttgt 1020
gaaaattctg gacacatttg agaagctgaa agatctattc actgagctgc agaagaagat 1080
ctatgtcatt gagggcacaa gcaaacagga cctgacttcc ttcaacatgg agctgtcctc 1140
cagcggcatc agtgctgacc tcagcagggg ccatgcagtc gtggggcaag taggagccaa 1200
ggactgggct ggggggcttt ttgacctgaa ggcagacctg caggatgaca catttattgg 1260
gaatgaacca ttgacaccag aagtgagagc aggctatttg ggttacaccg tgacctggct 1320
gccctcccgg caaaagactt cgttgctggc ctcgggagcc cctcgatacc agcacatggg 1380
ccgagtgctg ctgttccaag agccacaggg cggaggacac tggagccagg tccagacaat 1440
ccatgggacc cagattggct cttatttcgg tggggagctg tgtggcgtcg acgtggacca 1500
agatggggag acagagctgc tgctgattgg tgccccactg ttctatgggg agcagagagg 1560
aggccgggtg tttatctacc agagaagaca gttgggggttt gaagaagtct cagagctgca 1620
ggggaccccc ggctacccac tcgggcggtt tggaggaagcc atcactgctc tgacagacat 1680
caacgggcgat gggctggtag acgtggctgt gggaggccct ctggaggagc aggggcctat 1740
gtacatcttc aatggggaggc acggggggct tagtccccag ccaagtcagc ggatagaagg 1800
gacccaagtg ctctcaggaa ttcagtggtt tggacgctcc atccatgggg tgaaggacct 1860
tgaaggggat ggcttggcag atgtggctgt gggggctgag agccagatga tcgtgctgag 1920
ctcccggcco gtggtggata tggtcaccct gatgtccttc tctccagctg agatcccagt 1980
gcatgaagtg gagtgctcct attcaaccag taacaagatg aaagaaggag ttaatatcac 2040
aatctgtttc cagatcaagt ctctctaccc ccagttcaca ggccgcctgg ttgccaatct 2100
cacttacact ctgcagctgg atggccaccg gaccagaaga cgggggttgt tcccaggagg 2160
gagacatgaa ctcagaagga atatagctgt caccaccagc atgtcatgca ctgacttctc 2220

```
atttcatttc ccggtatgtg ttcaagacct catctccccc atcaatgttt ccctgaattt 2280
ctctctttgg gaggaggaag ggacaccgag ggaccaaagg gcgcagggca aggacatacc 2340
gccatcctg agaccctccc tgcactcgga aacctgggag atccctttg agaagaactg 2400
tggggaggac aagaagtgtg aggcaaactt aggcaaactt ttctctcctg caagatccag 2460
agccctgcgt ctaactgctt ttgccagcct ctctgtggag ctgagcctga gtaacttgga 2520
agaagatgct tactgggtcc agctggacct gcacttcccc ccgggactct ccttccgcaa 2580
ggtggagatg ctgaagcccc atagccagat acctgtgagc tgcgaggagc ttcctgaaga 2640
gtccaggctt ctgtccaggg cattatcttg caatgtgagc tctccatct tcaaagcagg 2700
ccactcggtt gctctgcaga tgatgtttaa tacactggta aacagctcct gggggggactc 2760
ggttgaattg cacgccaatg tgacctgtaa caatgaggac tcagacctcc tggaggacaa 2820
ctcagccact accatcatcc ccatcctgca ccccatcaac atcctcatcc aggaccaaga 2880
agactccaca ctctatgtca gtttcacccc caaaggcccc aagtaccacc aagtcaagca 2940
catgtaccag gtgaggatcc agccttccat ccacgaccac aacataccca ccctggaggc 3000
tgtggttggg gtgccacagc ctcccagcga ggggcccatc acacaccagt ggagcgtgca 3060
gatggagcct cccgtgccct gccactatga ggatctggag aggctcccgg atgcagctga 3120
gccttgtctc cccggagccc tgttccgctg ccctgttgtc ttcaggcagg agatctcgt 3180
ccaagtgatc gggactctgg agctggtggg agagatcgag gcctcttcca tgttcagcct 3240
ctgcagctcc ctctccatct ccttcaacag cagcaagcat ttccacctct atggcagcaa 3300
cgcctccctg gccaggttg tcatgaaggt tgacgtggtg tatgagaagc agatgctcta 3360
cctctacgtg ctgagcggca tcggggggct gctgctgtc ctgctcattt tcatagtgct 3420
gtacaaggtt ggtttcttca aacggaacct gaaggagaag atggaggctg gcagaggtgt 3480
cccgaatgga atccctgcag aagactctga gcagctggca tctgggcaag aggctgggga 3540
tccggctgc ctgaagcccc tccatgagaa ggactctgag agtggtggtg gcaaggactg 3600
agtccaggcc tgtgaggtgc agagtgccca gaactggact caggatgccc agggccactc 3660
tgcctctgcc tgcattctgc cgtgtgccct cgggcgagtc actgcctctc cctggcctc 3720
agtttcccta tctcgaacat ggaactcatt cctcgaatgt cctttgcag gctcataggg 3780
aagacctgct gagggaccag ccaagagggc tgcaaaagtg agggcttgtc attaccagac 3840
ggttcaccag cctctcttgg ttccttcctt ggaagagaat gtctgatcta aatgtggaga 3900
aactgtagtc tcaggaccta gggatgttct ggccctcacc cctgccctgg gatgtccaca 3960
gatgcctcca cccccagaa cctgtccttg cacactcccc tgcactggag tccagtctct 4020
tctgctggca gaaagcaaat gtgacctgtg tcactacgtg actgtggcac acgccttgtt 4080
cttggccaaa gaccaaattc cttggcatgc cttccagcac cctgcaaat gagaccctcg 4140
tggccttccc cagcctcttc tagagccgtg atgcctccct gttgaagctc tggtgacacc 4200
agcctttctc ccaggccagg ctccttcctg tcttcctgca ttcaccagga cagctccctc 4260
tgcctgaacc ttccatctcg cccacccctc cttccttgac cagcagatcc cagctcacgt 4320
cacacacttg gttgggtcct cacatctttc acacttccac caccctgcac tactccctca 4380
aagcacacgt catgttttctt catccggcag cctggatgtt ttttccctgt ttaatgattg 4440
acgtacttag cagctatctc tcagtgaact gtgagggtaa aggctatact tgtcttgttc 4500
accttgggat gacgccgcat gatatgtcag ggcgtgggac atctagtagg tgcttgacat 4560
aatttcactg aattaatgac agagccagtg ggaagataca gaaaaagagg gccgggggctg 4620
ggcgcggtgg ttcacgcctg taatcccagc actttgggag gccaaggagg gtggatcacc 4680
tgaggtcagg agttagaggc cagcctggcg aaacccatc tctactaaaa atacaaaatc 4740
caggcgtggt ggcacacacc tgtagtccca gctactcagg aggttgaggt aggagaattg 4800
cttgaacctg ggaggtggag gttgcagtga gccagagatt cgccattgca ctccagcctg 4860
ggcaacacag cgagactccg tctcaaggaa aaaataaaaa taaaaagcgg gcacgggccc 4920
ggacatcccc accttggcag gctgtcttct caggctctgc cctgccctag ctccacaccc 4980
tctcccagga cccatcacgc ctgtgcagtg gccccccacag aaagactgag ctcaaggtgg 5040
gaaccacgtc tgctaacttg gagcccccagt gccaagcaca gtgcctgcat gtatttatcc 5100
aataaatgtg aaattctgtc caaaaaaaaa aaa                             5133
```

```
<210> 2
<211> 1170
<212> PRT
<213> Homo sapiens

<400> 2
Met Lys Asp Ser Cys Ile Thr Val Met Ala Met Ala Leu Leu Ser Gly
1               5                   10                  15
Phe Phe Phe Phe Ala Pro Ala Ser Ser Tyr Asn Leu Asp Val Arg Gly
            20                  25                  30
Ala Arg Ser Phe Ser Pro Pro Arg Ala Gly Arg His Phe Gly Tyr Arg
```

```
         35                      40                    45
Val Leu Gln Val Gly Asn Gly Val Ile Val Gly Ala Pro Gly Glu Gly
    50                      55                    60
Asn Ser Thr Gly Ser Leu Tyr Gln Cys Gln Ser Gly Thr Gly His Cys
65                      70                    75                    80
Leu Pro Val Thr Leu Arg Gly Ser Asn Tyr Thr Ser Lys Tyr Leu Gly
                    85                    90                    95
Met Thr Leu Ala Thr Asp Pro Thr Asp Gly Ser Ile Leu Ala Cys Asp
                100                   105                   110
Pro Gly Leu Ser Arg Thr Cys Asp Gln Asn Thr Tyr Leu Ser Gly Leu
    115                   120                   125
Cys Tyr Leu Phe Arg Gln Asn Leu Gln Gly Pro Met Leu Gln Gly Arg
    130                   135                   140
Pro Gly Phe Gln Glu Cys Ile Lys Gly Asn Val Asp Leu Val Phe Leu
145                   150                   155                   160
Phe Asp Gly Ser Met Ser Leu Gln Pro Asp Glu Phe Gln Lys Ile Leu
                165                   170                   175
Asp Phe Met Lys Asp Val Met Lys Lys Leu Ser Asn Thr Ser Tyr Gln
                180                   185                   190
Phe Ala Ala Val Gln Phe Ser Thr Ser Tyr Lys Thr Glu Phe Asp Phe
    195                   200                   205
Ser Asp Tyr Val Lys Arg Lys Asp Pro Asp Ala Leu Leu Lys His Val
    210                   215                   220
Lys His Met Leu Leu Leu Thr Asn Thr Phe Gly Ala Ile Asn Tyr Val
225                   230                   235                   240
Ala Thr Glu Val Phe Arg Glu Glu Leu Gly Ala Arg Pro Asp Ala Thr
                245                   250                   255
Lys Val Leu Ile Ile Ile Thr Asp Gly Glu Ala Thr Asp Ser Gly Asn
                260                   265                   270
Ile Asp Ala Ala Lys Asp Ile Ile Arg Tyr Ile Ile Gly Ile Gly Lys
    275                   280                   285
His Phe Gln Thr Lys Glu Ser Gln Glu Thr Leu His Lys Phe Ala Ser
    290                   295                   300
Lys Pro Ala Ser Glu Phe Val Lys Ile Leu Asp Thr Phe Glu Lys Leu
305                   310                   315                   320
Lys Asp Leu Phe Thr Glu Leu Gln Lys Lys Ile Tyr Val Ile Glu Gly
                325                   330                   335
Thr Ser Lys Gln Asp Leu Thr Ser Phe Asn Met Glu Leu Ser Ser Ser
    340                   345                   350
Gly Ile Ser Ala Asp Leu Ser Arg Gly His Ala Val Val Gly Ala Val
    355                   360                   365
Gly Ala Lys Asp Trp Ala Gly Gly Phe Leu Asp Leu Lys Ala Asp Leu
    370                   375                   380
Gln Asp Asp Thr Phe Ile Gly Asn Glu Pro Leu Thr Pro Glu Val Arg
385                   390                   395                   400
Ala Gly Tyr Leu Gly Tyr Thr Val Thr Trp Leu Pro Ser Arg Gln Lys
                405                   410                   415
Thr Ser Leu Leu Ala Ser Gly Ala Pro Arg Tyr Gln His Met Gly Arg
                420                   425                   430
Val Leu Leu Phe Gln Glu Pro Gln Gly Gly Gly His Trp Ser Gln Val
    435                   440                   445
Gln Thr Ile His Gly Thr Gln Ile Gly Ser Tyr Phe Gly Gly Glu Leu
    450                   455                   460
Cys Gly Val Asp Val Asp Gln Asp Gly Glu Thr Glu Leu Leu Leu Ile
465                   470                   475                   480
Gly Ala Pro Leu Phe Tyr Gly Glu Gln Arg Gly Gly Arg Val Phe Ile
                485                   490                   495
Tyr Gln Arg Arg Gln Leu Gly Phe Glu Glu Val Ser Glu Leu Gln Gly
    500                   505                   510
Asp Pro Gly Tyr Pro Leu Gly Arg Phe Gly Glu Ala Ile Thr Ala Leu
    515                   520                   525
```

```
Thr Asp Ile Asn Gly Asp Gly Leu Val Asp Val Ala Val Gly Ala Pro
    530                     535                 540
Leu Glu Glu Gln Gly Ala Val Tyr Ile Phe Asn Gly Arg His Gly Gly
545                     550                 555                 560
Leu Ser Pro Gln Pro Ser Gln Arg Ile Glu Gly Thr Gln Val Leu Ser
                565                 570                 575
Gly Ile Gln Trp Phe Gly Arg Ser Ile His Gly Val Lys Asp Leu Glu
            580                 585                 590
Gly Asp Gly Leu Ala Asp Val Ala Val Gly Ala Glu Ser Gln Met Ile
        595                 600                 605
Val Leu Ser Ser Arg Pro Val Val Asp Met Val Thr Leu Met Ser Phe
    610                 615                 620
Ser Pro Ala Glu Ile Pro Val His Glu Val Glu Cys Ser Tyr Ser Thr
625                 630                 635                 640
Ser Asn Lys Met Lys Glu Gly Val Asn Ile Thr Ile Cys Phe Gln Ile
                645                 650                 655
Lys Ser Leu Tyr Pro Gln Phe Gln Gly Arg Leu Val Ala Asn Leu Thr
            660                 665                 670
Tyr Thr Leu Gln Leu Asp Gly His Arg Thr Arg Arg Arg Gly Leu Phe
        675                 680                 685
Pro Gly Gly Arg His Glu Leu Arg Arg Asn Ile Ala Val Thr Thr Ser
    690                 695                 700
Met Ser Cys Thr Asp Phe Ser Phe His Phe Pro Val Cys Val Gln Asp
705                 710                 715                 720
Leu Ile Ser Pro Ile Asn Val Ser Leu Asn Phe Ser Leu Trp Glu Glu
                725                 730                 735
Glu Gly Thr Pro Arg Asp Gln Arg Ala Gln Gly Lys Asp Ile Pro Pro
            740                 745                 750
Ile Leu Arg Pro Ser Leu His Ser Glu Thr Trp Glu Ile Pro Phe Glu
    755                 760                 765
Lys Asn Cys Gly Glu Asp Lys Lys Cys Glu Ala Asn Leu Arg Val Ser
    770                 775                 780
Phe Ser Pro Ala Arg Ser Arg Ala Leu Arg Leu Thr Ala Phe Ala Ser
785                 790                 795                 800
Leu Ser Val Glu Leu Ser Leu Ser Asn Leu Glu Glu Asp Ala Tyr Trp
                805                 810                 815
Val Gln Leu Asp Leu His Phe Pro Pro Gly Leu Ser Phe Arg Lys Val
            820                 825                 830
Glu Met Leu Lys Pro His Ser Gln Ile Pro Val Ser Cys Glu Glu Leu
        835                 840                 845
Pro Glu Glu Ser Arg Leu Leu Ser Arg Ala Leu Ser Cys Asn Val Ser
    850                 855                 860
Ser Pro Ile Phe Lys Ala Gly His Ser Val Ala Leu Gln Met Met Phe
865                 870                 875                 880
Asn Thr Leu Val Asn Ser Ser Trp Gly Asp Ser Val Glu Leu His Ala
                885                 890                 895
Asn Val Thr Cys Asn Asn Glu Asp Ser Asp Leu Leu Glu Asp Asn Ser
        900                 905                 910
Ala Thr Thr Ile Ile Pro Ile Leu Tyr Pro Ile Asn Ile Leu Ile Gln
    915                 920                 925
Asp Gln Glu Asp Ser Thr Leu Tyr Val Ser Phe Thr Pro Lys Gly Pro
    930                 935                 940
Lys Ile His Gln Val Lys His Met Tyr Gln Val Arg Ile Gln Pro Ser
945                 950                 955                 960
Ile His Asp His Asn Ile Pro Thr Leu Glu Ala Val Val Gly Val Pro
            965                 970                 975
Gln Pro Pro Ser Glu Gly Pro Ile Thr His Gln Trp Ser Val Gln Met
        980                 985                 990
Glu Pro Pro Val Pro Cys His Tyr Glu Asp Leu Glu Arg Leu Pro Asp
        995                 1000                1005
Ala Ala Glu Pro Cys Leu Pro Gly Ala Leu Phe Arg Cys Pro Val Val
```

```
     1010                    1015                    1020
Phe Arg Gln Glu Ile Leu Val Gln Val Ile Gly Thr Leu Glu Leu Val
1025                         1030                    1035                    1040
Gly Glu Ile Glu Ala Ser Ser Met Phe Ser Leu Cys Ser Ser Leu Ser
                    1045                    1050                    1055
Ile Ser Phe Asn Ser Ser Lys His Phe His Leu Tyr Gly Ser Asn Ala
                1060                    1065                    1070
Ser Leu Ala Gln Val Val Met Lys Val Asp Val Val Tyr Glu Lys Gln
          1075                    1080                    1085
Met Leu Tyr Leu Tyr Val Leu Ser Gly Ile Gly Gly Leu Leu Leu Leu
          1090                    1095                    1100
Leu Leu Ile Phe Ile Val Leu Tyr Lys Val Gly Phe Phe Lys Arg Asn
1105                    1110                    1115                    1120
Leu Lys Glu Lys Met Glu Ala Gly Arg Gly Val Pro Asn Gly Ile Pro
                    1125                    1130                    1135
Ala Glu Asp Ser Glu Gln Leu Ala Ser Gly Gln Glu Ala Gly Asp Pro
               1140                    1145                    1150
Gly Cys Leu Lys Pro Leu His Glu Lys Asp Ser Glu Ser Gly Gly Gly
          1155                    1160                    1165
Lys Asp
    1170
```

<210> 3
<211> 4740
<212> DNA
<213> Homo sapiens

<400> 3

```
gaattccgtg gttcctcagt ggtgcctgca acccctggtt cacctccttc caggttctgg    60
ctccttccag ccatggctct cagagtcctt ctgttaacag ccttgacctt atgtcatggg   120
ttcaacttgg acactgaaaa cgcaatgacc ttccaagaga acgcaagggg cttcgggcag   180
agcgtggtcc agcttcaggg atccagggtg gtggttggag cccccagga gatagtggct     240
gccaaccaaa ggggcagcct ctaccagtgc gactacagca caggctcatg cgagcccatc   300
cgcctgcagg tccccgtgga ggccgtgaac atgtccctgg gcctgtccct ggcagccacc   360
accagcccc ctcagctgct ggctgtggt cccaccgtgc accgaacttg cagtgagaac      420
acgtatgtga aagggctctg cttcctgttt ggcatccaac tacggcagca gcccagaag     480
ttcccagagg ccctccgagg gtgtcctcaa gaggatagtg acattgcctt cttgattgat     540
ggctctggta gcatcatccc acatgacttt cggcggatga aggagtttgt ctcaactgcg     600
atggagcaat taaaaaagtc caaaaccttg ttctctttga tgcagtactc tgaagaattc     660
cggattcact ttacctttcaa agagttccag aacaaccota acccaagatc actggtgaag    720
ccaataacgc agctgcttgg gcggacacac acggccacgg gcatccgcaa agtggtacga     780
gagctgttta acatcaccaa cggagcccga aagaatgcct ttaagatcct agttgtcatc     840
acggatggag aaaagtttgg cgatccctg ggatatgagg atgtcaatcc tgaggcagac      900
agagagggag tcattcgcta cgtcattggg gtgggagatg ccttccgcag tgagaaatcc     960
cgccaagagc ttaataccat cgcatccaag ccgcctgctg atcacgtgtt ccaggtgaat    1020
aactttgagg ctctgaagac cattcagaac cagcttcggg agaagatctt tgcgatcgag    1080
ggtactcaga caggaagtag cagctccttt gagcatgaga tgtctcagga aggcttcagc    1140
gctgccatca cctctaatgg ccccttgctg agcactgtgg ggagctatga ctgggctggt    1200
ggagtctttc tatataccat aaaggagaaa gcaccttca tcaacatgac cagagtggat     1260
tcagacatga atgatgctta cttgggttat gctgccgcca tcatcttacg gaaccgggtg    1320
caaagcctgg ttctgggggc acctcgatat cagcacatcg gcctggtagc gatgttcagg    1380
cagaacactg gcatgtggga gtccaacgct aatgtcaagg gcacccagat cggcgcctac    1440
ttcggggcct ccctctgctc cgtcgtacgtg gacagcaacg gcagcaccga cctggtcctc    1500
atcggggccc cccattacta cgagcagacc cgaggggggcc aggtgtccgt gtgcccccttg   1560
cccaggggc agagggctcg gtggcagtgt gatgctgttc tctacgggga gcagggcaa      1620
cctgggggcc gctttggggc agccctaaca gtgctggggga acgtaaatgg ggacaagctg   1680
acggacgtgg ccattggggc cccagaggag gaggacaacc ggggtgctgt ttacctgttt    1740
cacggaacct caggatctg g catcagcccc tcccataggcc agcggatagc aggctccaag   1800
ctctctccca ggctccagta tttttggtcag tcactgagtg ggggccagga cctcacaatg    1860
gatggactgg tagacctgac tgtaggagcc caggggcacg tgctgctgct caggtcccag    1920
```

```
ccagtactga gagtcaaggc aatcatggag ttcaatccca gggaagtggc aaggaatgta 1980
tttgagtgta atgatcaggt ggtgaaaggc aaggaagccg gagaggtcag agtctgcctc 2040
catgtccaga agagcacacg ggatcggcta agagaaggac agatccagag tgttgtgact 2100
tatgacctgg ctctggactc cggccgccca cattcccgcg ccgtcttcaa tgagacaaag 2160
aacagcacac gcagacagac acaggtcttg gggctgaccc agacttgtga gaccctgaaa 2220
ctacagttgc cgaattgcat cgaggaccca gtgagcccca ttgtgctgcg cctgaacttc 2280
tctctggtgg gaacgccatt gtctgctttc gggaacctcc ggccagtgct ggcggaggat 2340
gctcagagac tcttcacagc cttgtttccc tttgagaaga attgtggcaa tgacaacatc 2400
tgccaggatg acctcagcat caccttcagt ttcatgagcc tggactgcct cgtggtgggt 2460
gggccccggg agttcaacgt gacagtgact gtgagaaatg atggtgagga ctcctacagg 2520
acacaggtca ccttcttctt cccgcttgac ctgtcctacc ggaaggtgtc cacactccag 2580
aaccagcgct cacagcgatc ctggcgcctg gcctgtgagt ctgcctcctc caccgaagtg 2640
tctggggcct tgaagagcac cagctgcagc ataaaccacc ccatcttccc ggaaaactca 2700
gaggtcacct ttaatatcac gtttgatgta gactctaagg cttcccttgg aaacaaactg 2760
ctcctcaagg ccaatgtgac cagtgagaac aacatgccca gaaccaacaa aaccgaattc 2820
caactggagc tgccggtgaa atatgctgtc tacatggtgg tcaccagcca tggggtctcc 2880
actaaatatc tcaacttcac ggcctcagag aataccagtc gggtcatgca gcatcaatat 2940
caggtcagca acctggggca gaggagcctc cccatcagcc tggtgttctt ggtgcccgtc 3000
cggctgaacc agactgtcat atgggaccgc cccagtgca cctttcccga gaacctctcg 3060
agtacgtgcc acaccaagga gcgcttgccc tctcactccg actttctggc tgagcttcgg 3120
aaggcccccg tggtgaactg ctccatcgct gtctgccaga gaatccagtg tgacatcccg 3180
ttctttggca tccaggaaga attcaatgct acctcaaag gcaacctctc gtttgactgg 3240
tacatcaaga cctcgcataa ccacctcctg atcgtgagca cagctgagat cttgtttaac 3300
gattccgtgt tcaccctgct gccgggacag gggcgtttg tgaggtccca gacggagacc 3360
aaagtggagc cgttcgaggt ccccaacccc ctgccgctca tcgtgggcag ctctgtcggg 3420
ggactgctgc tcctggccct catcaccgcc gcgctgtaca agctcggctt cttcaagcgg 3480
caatacaagg acatgatgag tgaaggggt ccccgggggg ccgaacccca gtagcggctc 3540
cttcccgaca gagctgcctc tcggtggcca gacgactct gcccagacca cacgtagccc 3600
ccaggctgct ggacacgtcg gacagcgaag tatcccgac aggacgggct tgggcttcca 3660
tttgtgtgtg tgcaagtgtg tatgtgcgtg tgtgcgagtg tgtgcaagtg tctgtgtgca 3720
agtgtgtgca cgtgtgcgtg tgcgtgcatg tgcactcgca cgcccatgtg tgagtgtgtg 3780
caagtatgtg agtgtgtcca gtgtgtgtgc gtgtgtcatg tgtgtgcag tgtgtgcatg 3840
tgtgcgagtg tgtgcatgtg tgtgctcagg ggctgtggct cacgtgtgtg actcagagtg 3900
tctctggcgt gtgggtaggt gacggcagcg tagcctctcc ggcagaaggg aactgcctgg 3960
gctcccttgt gcgtgggtaa gccgctgctg ggttttcctc cgggagaggg gacggtcaat 4020
cctgtgggtg aagagagagg gaaacacagc agcatctctc cactgaaaga agtgggactt 4080
cccgtcgcct gcgagcctgc ggcctgctag gctgggatgg atactccatg 4140
agaaaagccg tgggtggaac caggagcctc ctccacacca gcgctgatgc ccaataaaga 4200
tgcccactga ggaatcatga agcttccttt ctggattcat ttattattc aatgtgactt 4260
taattttttg gatgataag cctgtctatg atacaaaat cacaaggcat tcaagtgtac 4320
agtgaaaagt ctccctttcc agatattcaa gtcacctcct taaaggtagt caagattgtg 4380
ttttgaggtt tccttcagac agattccagg cgatgtgcaa gtgtatgcac gtgtgcacac 4440
accacacaca tacacacaca caagcttttt tacacaaatg gtagcatact ttatattggt 4500
ctgtatcttg cttttttcca ccaatatttc tcagacatcg gttcatatta agacataaat 4560
tactttttca ttcttttata ccgctgcata gtattccatt gtgtgagtgt accataatgt 4620
atttaaccag tcttcttttg atatactatt ttcatctctt gttattgcat ctgctgagtt 4680
aatataca atatatgtca aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 4740
```

<210> 4
<211> 1152
<212> PRT
<213> Homo sapiens

<400> 4

```
Met Ala Leu Arg Val Leu Leu Leu Thr Ala Leu Thr Leu Cys His Gly
1               5                   10                  15
Phe Asn Leu Asp Thr Glu Asn Ala Met Thr Phe Gln Glu Asn Ala Arg
            20                  25                  30
Gly Phe Gly Gln Ser Val Val Gln Leu Gln Gly Ser Arg Val Val Val
        35                  40                  45
```

```
Gly Ala Pro Gln Glu Ile Val Ala Ala Asn Gln Arg Gly Ser Leu Tyr
    50                      55                  60
Gln Cys Asp Tyr Ser Thr Gly Ser Cys Glu Pro Ile Arg Leu Gln Val
65                  70                  75                  80
Pro Val Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Thr
                85                  90                  95
Thr Ser Pro Pro Gln Leu Leu Ala Cys Gly Pro Thr Val His Gln Thr
        100                 105                 110
Cys Ser Glu Asn Thr Tyr Val Lys Gly Leu Cys Phe Leu Phe Gly Ser
        115                 120                 125
Asn Leu Arg Gln Gln Pro Gln Lys Phe Pro Glu Ala Leu Arg Gly Cys
    130                 135                 140
Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser
145                 150                 155                 160
Ile Ile Pro His Asp Phe Arg Arg Met Lys Glu Phe Val Ser Thr Val
                165                 170                 175
Met Glu Gln Leu Lys Lys Ser Lys Thr Leu Phe Ser Leu Met Gln Tyr
        180                 185                 190
Ser Glu Glu Phe Arg Ile His Phe Thr Phe Lys Glu Phe Gln Asn Asn
    195                 200                 205
Pro Asn Pro Arg Ser Leu Val Lys Pro Ile Thr Gln Leu Leu Gly Arg
    210                 215                 220
Thr His Thr Ala Thr Gly Ile Arg Lys Val Val Arg Glu Leu Phe Asn
225                 230                 235                 240
Ile Thr Asn Gly Ala Arg Lys Asn Ala Phe Lys Ile Leu Val Val Ile
                245                 250                 255
Thr Asp Gly Glu Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile
        260                 265                 270
Pro Glu Ala Asp Arg Glu Gly Val Ile Arg Tyr Val Ile Gly Val Gly
    275                 280                 285
Asp Ala Phe Arg Ser Glu Lys Ser Arg Gln Glu Leu Asn Thr Ile Ala
    290                 295                 300
Ser Lys Pro Pro Arg Asp His Val Phe Gln Val Asn Asn Phe Glu Ala
305                 310                 315                 320
Leu Lys Thr Ile Gln Asn Gln Leu Arg Glu Lys Ile Phe Ala Ile Glu
                325                 330                 335
Gly Thr Gln Thr Gly Ser Ser Ser Ser Phe Glu His Glu Met Ser Gln
        340                 345                 350
Glu Gly Phe Ser Ala Ala Ile Thr Ser Asn Gly Pro Leu Leu Ser Thr
        355                 360                 365
Val Gly Ser Tyr Asp Trp Ala Gly Gly Val Phe Leu Tyr Thr Ser Lys
370                 375                 380
Glu Lys Ser Thr Phe Ile Asn Met Thr Arg Val Asp Ser Asp Met Asn
385                 390                 395                 400
Asp Ala Tyr Leu Gly Tyr Ala Ala Ala Ile Ile Leu Arg Asn Arg Val
                405                 410                 415
Gln Ser Leu Val Leu Gly Ala Pro Arg Tyr Gln His Ile Gly Leu Val
        420                 425                 430
Ala Met Phe Arg Gln Asn Thr Gly Met Trp Glu Ser Asn Ala Asn Val
    435                 440                 445
Lys Gly Thr Gln Ile Gly Ala Tyr Phe Gly Ala Ser Leu Cys Ser Val
    450                 455                 460
Asp Val Asp Ser Asn Gly Ser Thr Asp Leu Val Leu Ile Gly Ala Pro
465                 470                 475                 480
His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro Leu
                485                 490                 495
Pro Arg Gly Arg Ala Arg Trp Gln Cys Asp Ala Val Leu Tyr Gly Glu
            500                 505                 510
Gln Gly Gln Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu Gly
    515                 520                 525
Asp Val Asn Gly Asp Lys Leu Thr Asp Val Ala Ile Gly Ala Pro Gly
```

```
         530                       535                      540
Glu Glu Asp Asn Arg Gly Ala Val Tyr Leu Phe His Gly Thr Ser Gly
545                       550                      555              560
Ser Gly Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Ser Lys Leu
                    565                       570                      575
Ser Pro Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln Asp
               580                       585                      590
Leu Thr Met Asp Gly Leu Val Asp Leu Thr Val Gly Ala Gln Gly His
          595                       600                      605
Val Leu Leu Leu Arg Ser Gln Pro Val Leu Arg Val Lys Ala Ile Met
     610                       615                      620
Glu Phe Asn Pro Arg Glu Val Ala Arg Asn Val Phe Glu Cys Asn Asp
625                       630                      635              640
Gln Val Val Lys Gly Lys Glu Ala Gly Glu Val Arg Val Cys Leu His
                    645                       650                      655
Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln Ser
               660                       665                      670
Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser Arg
          675                       680                      685
Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln Val
     690                       695                      700
Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro Asn
705                       710                      715              720
Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe Ser
                    725                       730                      735
Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val Leu
               740                       745                      750
Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu Lys
          755                       760                      765
Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr Phe
     770                       775                      780
Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu Phe
785                       790                      795              800
Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg Thr
                    805                       810                      815
Gln Val Thr Phe Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val Ser
               820                       825                      830
Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys Glu
          835                       840                      845
Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser Cys
     850                       855                      860
Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe Asn
865                       870                      875              880
Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu Leu
                    885                       890                      895
Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn Lys
               900                       905                      910
Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met Val
          915                       920                      925
Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala Ser
     930                       935                      940
Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn Leu
945                       950                      955              960
Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val Arg
                    965                       970                      975
Leu Asn Gln Thr Val Ile Trp Asp Arg Pro Gln Val Thr Phe Ser Glu
               980                       985                      990
Asn Leu Ser Ser Thr Cys His Thr Lys Glu Arg Leu Pro Ser His Ser
          995                      1000                     1005
Asp Phe Leu Ala Glu Leu Arg Lys Ala Pro Val Val Asn Cys Ser Ile
     1010                      1015                     1020
```

Ala Val Cys Gln Arg Ile Gln Cys Asp Ile Pro Phe Phe Gly Ile Gln
1025   1030   1035   1040
Glu Glu Phe Asn Ala Thr Leu Lys Gly Asn Leu Ser Phe Asp Trp Tyr
                    1045   1050   1055
Ile Lys Thr Ser His Asn His Leu Leu Ile Val Ser Thr Ala Glu Ile
                1060   1065   1070
Leu Phe Asn Asp Ser Val Phe Thr Leu Leu Pro Gly Gln Gly Ala Phe
          1075   1080   1085
Val Arg Ser Gln Thr Glu Thr Lys Val Glu Pro Phe Glu Val Pro Asn
      1090   1095   1100
Pro Leu Pro Leu Ile Val Gly Ser Ser Val Gly Gly Leu Leu Leu Leu
1105   1110   1115   1120
Ala Leu Ile Thr Ala Ala Leu Tyr Lys Leu Gly Phe Phe Lys Arg Gln
                    1125   1130   1135
Tyr Lys Asp Met Met Ser Glu Gly Gly Pro Pro Gly Ala Glu Pro Gln
                1140   1145   1150